

This listing of claims will replace all prior versions, and listings, of claims in the application:

Listing of Claims:

Claim 1 (currently amended): An isolated carotenoid overproducing *E. coli* comprising the genes encoding a functional carotenoid enzymatic biosynthetic pathway consisting of the genes *dxs*, *dxr*, *ygbP*, *ychB*, *ygbB*, *lytB*, *idi*, *ispA*, *ispB*, *crtE*, *crtB*, *crtI*, and *crtY*; wherein the *dxs*, *idi* and *ygbBP* genes are overexpressed; ~~and wherein the *yjeR* gene is down regulated by gene disruption to have the~~ nucleotide sequence set forth in SEQ ID NO:63; and wherein the *dxs*, the *idi*, *ychB*, *ispA*, *ispB* and *ygbBP* and *yjeR* genes are derived from either *E. coli* or *Methylobacter*; the *dxs* gene is derived from *E. coli* or is the nucleotide sequence set forth in SEQ ID NO:13; the *dxr* gene is derived from *E. coli* or is the nucleotide sequence set forth in SEQ ID NO:17; the *lytB* gene is derived from *E. coli* or is the nucleotide sequence set forth in SEQ ID NO:15; the *crtE* gene is the nucleotide sequence set forth in SEQ ID NO:1; the *crtB* gene is the nucleotide sequence set forth in SEQ ID NO:9; the *crtI* gene is the nucleotide sequence set forth in SEQ ID NO:7; and the *crtY* gene is the nucleotide sequence set forth in SEQ ID NO:5.

Claim 2 (currently amended): An isolated carotenoid overproducing *E. coli* comprising genes encoding a functional carotenoid enzymatic biosynthetic pathway consisting of the genes *dxs*, *dxr*, *ygbP*, *ychB*, *ygbB*, *lytB*, *idi*, *ispA*, *ispB*, *crtE*, *crtB*, *crtI*, and *crtY*; wherein the *dxs*, *idi*, *ygbBP* and *ispB* genes are overexpressed; ~~and~~ wherein the *dxs*, the *ychB*, *ispA*, *idi*, *ygbBP* and *ispB* genes are derived from either *E. coli* or *Methylobacter*; the *dxs* gene is derived from *E. coli* or is the nucleotide sequence set forth in SEQ ID NO:13; the *dxr* gene is derived from *E. coli* or is the nucleotide sequence set forth in SEQ ID NO:17; the *lytB* gene is derived from *E. coli* or is the nucleotide sequence set forth in SEQ ID NO:15; the *crtE* gene is the nucleotide sequence set forth in SEQ ID NO:1; the *crtB* gene is the nucleotide sequence set forth in SEQ ID NO:9; the *crtI* gene is the nucleotide sequence set forth in SEQ ID NO:7; and the *crtY* gene is the nucleotide sequence set forth in SEQ ID NO:5.

Claim 3 (currently amended): The carotenoid overproducing *E. coli* of Claim 1 or 2 wherein the *lytB* and *dxr* genes are ~~gene is~~ optionally overexpressed ~~and wherein the *lytB* and *dxr* genes are derived from *E. coli* and *Methylobionas*.~~

Claims 4-8 (canceled)

Claim 9 (currently amended): The carotenoid overproducing *E. coli* of either of Claims 1 or 2 wherein the *dxs*, *idi*, *ispB* and *ygbBP* genes are under the control of a strong promoter.

Claim 10 (previously presented): The carotenoid overproducing *E. coli* of Claim 9 wherein the strong promoter is selected from the group consisting of *lac*, *ara*, *tet*, *trp*, λP_L , λP_R , *T7*, *tac*, P_{T5} , and *trc*.

Claim 11 (previously presented): The carotenoid overproducing *E. coli* of either of Claims 1 or 2 wherein the *dxs*, *idi*, *ispB* and *ygbBP* genes are integrated in multicopy in the bacterial chromosome.

Claim 12 (previously presented): The carotenoid overproducing *E. coli* of either of Claims 1 or 2 wherein the *dxs*, *idi*, *ispB* and *ygbBP* genes are present in multicopy in the bacteria on one or more plasmids.

Claims 13-14 (canceled)

Claim 15 (currently amended): The carotenoid overproducing *E. coli* of either of Claims 1 or 2 wherein the *dxs*, *idi*, *ispB*, *ygbBP* and *lytB* genes are chromosomally integrated into the host cell genome.

Claim 16 (previously presented): A carotenoid overproducing *E. coli* selected from the group consisting of: a strain having the ATCC identification number PTA-4807 and a strain having the ATCC identification number PTA-4823.

Claim 17 (withdrawn): A method for the production of a carotenoid comprising:

- a) growing the carotenoid overproducing bacteria of any of Claims 1-5, the bacteria overexpressing at least one gene selected from the group consisting of *dxs*, *idi ygbBP*, *ispB*, *lytB*, *dxr*, wherein *yjeR* is optionally downregulated, for a time sufficient to produce a carotenoid; and
- b) optionally recovering the carotenoid from the carotenoid overproducing bacteria of step (a).

Claim 18 (withdrawn): A method according to Claim 17 wherein the carotenoid is selected from the group consisting of antheraxanthin, adonixanthin, astaxanthin, canthaxanthin, capsorubrin, β -cryptoxanthin, didehydrolycopene, didehydrolycopene, β -carotene, ζ -carotene, δ -carotene, γ -carotene, keto- γ -carotene, ψ -carotene, ϵ -carotene, β,ψ -carotene, torulene, echinenone, gamma-carotene, zeta-carotene, alpha-cryptoxanthin, diatoxanthin, 7,8-didehydroastaxanthin, fucoxanthin, fucoxanthinol, isorenieratene, β -isorenieratene lactucaxanthin, lutein, lycopene, neoxanthin, neurosporene, hydroxyneurosporene, peridinin, phytoene, rhodopin, rhodopin glucoside, siphonaxanthin, spheroidene, spheroidenone, spirilloxanthin, uriolide, uriolide acetate, violaxanthin, zeaxanthin- β -diglucoside, zeaxanthin, and C30-carotenoids.

Claim 19 (withdrawn): A method according to Claim 18 wherein the carotenoid is produced at a level of at least about 6 mg per gram dry cell weight.

Claim 20 (withdrawn): A method according to Claim 18 wherein the bacteria is selected from the group consisting of *Agrobacterium*, *Erythrobacter*, *Chlorobium*, *Chromatium*, *Flavobacterium*, *Cytophaga*, *Rhodobacter*, *Rhodococcus*, *Streptomyces*, *Brevibacterium*, *Corynebacteria*, *Mycobacterium*, *Deinococcus*, *Paracoccus*, *Escherichia*, *Bacillus*, *Myxococcus*, *Salmonella*, *Yersinia*, *Erwinia*, *Pantoea*, *Pseudomonas*, *Sphingomonas*, *Methylomonas*, *Methylobacter*, *Methylococcus*, *Methylosinus*, *Methylomicrobium*, *Methylocystis*, *Alcaligenes*, *Synechocystis*, *Synechococcus*, *Anabaena*, *Thiobacillus*, *Methanobacterium*, *Klebsiella*, and *Myxococcus*.

Claim 21 (withdrawn): A method according to Claim 17 wherein the *dxs*, *idi*, *ygbBP*, *ispB* and *lytB* genes are under the control of a promoter selected from the group consisting of *lac*, *ara*, *tet*, *trp*, λP_L , λP_R , *T7*, P_{T5} , and *trc*.

Claim 23 (withdrawn): A method according to Claim 17 wherein the *dxs*, *idi*, *ispB*, *ygbBP* and *lytB* genes are integrated in multicopy in the bacterial chromosome.

Claim 24 (withdrawn): A method according to Claim 17 wherein the *dxs*, *idi*, *ispB*, *ygbBP* and *lytB* genes are in multicopy in the bacteria on one or more plasmids.

Claim 25 (withdrawn): A method according to Claim 17 wherein the *yjeR* gene is down regulated by gene disruption.

Claim 26 (withdrawn): A method according to Claim 25 wherein the disrupted *yjeR* gene has the nucleotide sequence as set forth in SEQ ID NO:63.

Claim 27 (withdrawn): A method according to Claim 17 wherein the *dxs*, *idi*, *ispB*, *ygbBP* and *lytB* genes are chromosomally integrated into the host cell genome.

Claim 28 (new): An isolated carotenoid overproducing *E. coli* comprising the genes encoding a functional carotenoid enzymatic biosynthetic pathway consisting of the genes *dxs*, *dxr*, *ygbP*, *ychB*, *ygbB*, *lytB*, *idi*, *ispA*, *ispB*, *crtE*, *crtB*, *crtI*, *crtY*, and *crtZ*; wherein the *dxs*, *idi* and *ygbBP* genes are overexpressed; the *yjeR* gene is down regulated by gene disruption to have the nucleotide sequence set forth in SEQ ID NO:63; the *idi*, *ychB*, *ispA*, *ispB* and *ygbBP* genes are derived from *E. coli*; the *dxs* gene is derived from *E. coli* or is the nucleotide sequence set forth in SEQ ID NO:13; the *dxr* gene is derived from *E. coli* or is the nucleotide sequence set forth in SEQ ID NO:17; the *lytB* gene is derived from *E. coli* or is the nucleotide sequence set forth in SEQ ID NO:15; the *crtE* gene is the nucleotide sequence set forth in SEQ ID NO:1; the *crtB* gene is the nucleotide sequence set forth in SEQ ID NO:9; the *crtI* gene is the nucleotide sequence set forth in SEQ ID NO:7; the *crtY* gene is the nucleotide sequence set forth in SEQ ID NO:5; and the *crtZ* gene is the nucleotide sequence set forth in SEQ ID NO:11.

Claim 29 (new): An isolated carotenoid overproducing *E. coli* comprising genes encoding a functional carotenoid enzymatic biosynthetic pathway consisting of the genes *dxs*, *dxr*, *ygbP*, *ychB*, *ygbB*, *lytB*, *idi*, *ispA*, *ispB*, *crtE*, *crtB*, *crtI*, *crtY*, and *crtZ*; wherein the *dxs*, *idi*, *ygbBP* and *ispB* genes are overexpressed; the *ychB*, *ispA*, *idi*, *ygbBP* and *ispB* genes are derived from *E. coli*; the *dxs* gene is derived from *E. coli* or is the nucleotide sequence set forth in SEQ ID NO:13; the *dxr* gene is derived from *E. coli* or is the nucleotide sequence set forth in SEQ ID NO:17; the *lytB* gene is derived from *E. coli* or is the nucleotide sequence set forth in SEQ ID NO:15; the *crtE* gene is the nucleotide sequence set forth in SEQ ID NO:1; the *crtB* gene is the nucleotide sequence set forth in SEQ ID NO:9; the *crtI* gene is the nucleotide sequence set forth in SEQ ID NO:7; the *crtY* gene is the nucleotide sequence set forth in SEQ ID NO:5; and the *crtZ* gene is the nucleotide sequence set forth in SEQ ID NO:11.